Microbial Source Tracking: Methods, Uses and Limitations

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Review Articles

- Sinton, I. W., R. K. Finlay, and D. J. Hannah. 1998. Distinguishing human from animal faecal contamination in water: a review. New Zealand J. of Marine and Freshwater Research **32**: 323-348.

- Simpson, J. M., J. W. Santo Domingo and D. J. Reasoner. 2002. Microbial Source Tracking: State of the Science. Environ. Science and Technology **36**(24):5279-5288.

Water Quality Assessment

<u>Clean Water Act (1972)</u>

Recreational waters should be "fishable and swimmable" Impairment of water quality may involve multiple pollutants or pollutant classes.

Impaired waterbody. Any waterbody of the United States that does not attain water quality standards (as defined in 40 CFR part 131) due to an individual pollutant, multiple pollutants, pollution, or an unknown cause of impairment.

TMDL Problem Sources

- **Point Sources: treatment plants, CAFOs**

- **Non-Point Sources : agriculture, forestry, wildlife and urban runoff**

- **Contamination Sources :   human vs animal**

     livestock vs wildlife

Microbial Source Tracking?

What is Microbial Source Tracking (MST)?

- A process of determining the host origin of fecal microbial pollution (bacteria, viruses or protozoa)

- Many potential MST methods require a host origin database to identify environmental isolates

- If just looking at bacteria, then it's bacterial source tracking (BST)

Basis of MST Method

- Bacteria with identical genetic fingerprints isolated from both the polluted site and the suspected animal source strongly suggests that the animal is the source of the pollution.

Why would MST work?

- Population biology

The intestinal bacteria of animal groups are expected to be different because of:

- Gut conditions
  - Temperature, food source, digestive system
- Natural selection
  - Competition for space and nutrients

- Epidemiology
  - Some subtypes or species have only been found in specific hosts

Assumptions

- Microbial species shows geographical structure

  i.e., clonal composition of populations differ among localities

Assumptions

- The clonal composition of the species isolated from environmental samples represents the clonal composition of the species responsible for the fecal inputs.

    i.e., fingerprints are stable in both primary and secondary habitats

Assumptions

- The clonal composition of populations is stable through time

    i.e., the same clones can be recovered from the same locality or host populations for "extended" periods of time

Assumptions

- The species exhibit some degree of host specificity

    i. e., high probability that particular clones are isolated from one host species, or group of species, than another

Fecal Coliforms

- **Grow on special medium at 44.5° C (115° F) after 24 hours**

- Consist of:
    - *Escherichia coli*
    - *Klebsiella pneumoniae*

Fecal Enterococci

- Grow on special medium at 41° C (106° F) after 48 hours
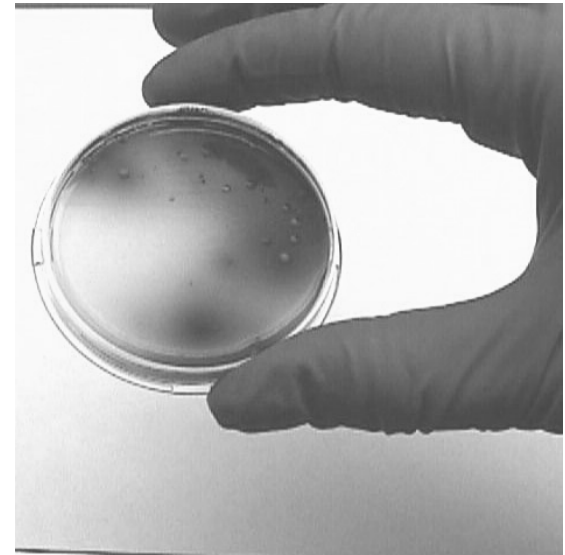- Consist of:

  Enterococcus avium

  Enterococcus faecalis

  Enterococcus faecium

  Enterococcus gallinarum

  Streptococcus bovis

  Streptococcus equinus

Microbial Source Tracking

Library = DNA "finger prints" database of bacterial isolates using the phenotypic or molecular methods.

1000s of isolates from water and suspected animal sources are required in the library.